sequence of SEQ ID NO: 2 from amino acid residue 32 to amino acid residue 330; (d) molecules complementary to (a), (b) or (c); and (e) degenerate nucleotide sequences of (a), (b), (c) or (d).

Please replace the paragraph on page 4, line 22 – page 5, line 2 with:

Within another aspect of the invention there is provided an expression vector comprising the following operably linked elements: a transcription promoter; a DNA segment selected from the group consisting of (a) polynucleotide molecules encoding a polypeptide having mannanase activity and comprising a sequence of nucleotides as shown in SEQ ID NO: 1 from nucleotide 94 to nucleotide 990; (b) species homologs of (a); (c) polynucleotide molecules that encode a polypeptide having mannanase activity that is at least 65% identical to the amino acid sequence of SEQ ID NO: 2 from amino acid residue 32 to amino acid residue 330; and (d) degenerate nucleotide sequences of (a), (b), or (c); and a transcription terminator.

Please replace the paragraph on page 5, lines 7-17 with:

Further aspects of the present invention provide an isolated polypeptide having mannanase activity selected from the group consisting of (a) polypeptide molecules comprising a sequence of amino acid residues as shown in SEQ ID NO:2 from amino acid residue 32 to amino acid residue 330; (b) species homologs of (a); and a fusion protein having mannanase activity comprising a first polypeptide part exhibiting mannanase activity and a second polypeptide part exhibiting cellulose binding function, the second polypeptide preferably being a cellulose binding domain (CBD), such as a fusion protein represented by SEQ ID NO:4.

Please replace the paragraph on page 24, line 27 – page 25, line 12 with:

The sequence of amino acids in positions 32-490 of SEQ ID NO: 2 is a mature mannanase sequence. The sequence of amino acids nos. 1-31 of SEQ ID NO: 2 is the signal peptide. It is believed that the subsequence of amino acids in positions 32-330 of SEQ ID NO: 2 is the catalytic domain of the mannanase enzyme and that the mature enzyme additionally comprises a linker in positions 331-342 and at least one C-terminal domain of unknown function in positions 343-490. Since the object of the present invention is to obtain a polypeptide which exhibits mannanase activity, the present invention relates to any mannanase enzyme comprising

the sequence of amino acids nos. 32-330 of SEQ ID NO: 2, i.e. a catalytical domain, optionally operably linked, either N-terminally or C-terminally, to one or two or more than two other domains of a different functionality. The domain having the subsequence of amino acids nos. 343-490 of SEQ ID NO: 2 is a domain of the mannanase enzyme of unknown function, this domain being highly homologous with similar domains in known mannanases, cf. example 1.

Please replace the paragraph on page 29, line 26 – page 30, line 28 with:

The present invention also provides mannanase polypeptides that are substantially homologous to the polypeptides of SEQ ID NO:2, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30 and SEQ ID NO:32, respectively, and species homologs (paralogs or orthologs) thereof. The term "substantially homologous" is used herein to denote polypeptides having 65%, preferably at least 70%, more preferably at least 75%, more preferably at least 80%, more preferably at least 85%, and even more preferably at least 90%, sequence identity to the sequence shown in amino acids nos. 32-330 or nos. 32-490 of SEQ ID NO:2 or their orthologs or paralogs; or to the sequence shown in amino acids nos. 32-344 or nos. 32-494 of SEQ ID NO:6 or their orthologs or paralogs; or to the sequence shown in amino acids nos. 32-362 or nos. 32-586 of SEQ ID NO:10 or their orthologs or paralogs; or to the sequence shown in amino acids nos. 33-331 of SEQ ID NO:12 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 166-488 or nos. 22-488 of SEQ ID NO:14 or their orthologs or paralogs; or to the sequence shown in amino acids nos. 68-369 or nos. 32-369 of SEQ ID NO:16 or their orthologs or paralogs; or to the sequence shown in amino acids nos. 1-305 of SEQ ID NO:18 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 1-132 of SEQ ID NO:20 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 29-320 of SEQ ID NO:22 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 29-188 of SEQ ID NO:24 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 301-625 or nos. 30-625 of SEQ ID NO:26 or their orthologs or paralogs; or to the sequence shown in amino acids nos. 166-496 or nos. 38-496 of SEQ ID NO:28 or their orthologs or paralogs; or to the sequence shown in amino acids nos. 26-361 of SEQ ID NO:30 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 593-903 or nos. 23-903 of SEQ ID NO:32 or their orthologs or paralogs.

198

Please replace the paragraph on page 30, line 29 – page 31, line 22 with:

Such polypeptides will more preferably be at least 95% identical, and most preferably 98% or more identical to the sequence shown in amino acids nos. 32-330 or nos. 32-490 of SEQ ID NO:2 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 32-344 or nos. 32-494 of SEQ ID NO:6 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 32-362 or nos. 32-586 of SEQ ID NO:10 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 33-331 of SEQ ID NO:12 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 166-488 or nos. 22-488 of SEQ ID NO:14 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 68-369 or nos. 32-369 of SEQ ID NO:16 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 1-305 of SEQ ID NO:18 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 1-132 of SEQ ID NO:20 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 29-320 of SEQ ID NO:22 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 29-188 of SEQ ID NO:24 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 301-625 or nos. 30-625 of SEQ ID NO:26 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 166-496 or nos. 38-496 of SEQ ID NO:28 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 26-361 of SEQ ID NO:30 or its orthologs or paralogs; or to the sequence shown in amino acids nos. 593-903 or nos. 23-903 of SEQ ID NO:32 or its orthologs or paralogs.

Please replace the paragraph on page 38, lines 8-21 with:

Using the methods discussed above, one of ordinary skill in the art can identify and/or prepare a variety of polypeptides that are substantially homologous to residues 32-330 or 32-490 of SEQ ID NO:2; or to residues 32-344 or 32-494 of SEQ ID NO:6; or to residues 32-362 or32-586 of SEQ ID NO:10; or to residues 33-331 of SEQ ID NO:12; or to residues 166-488 or 22-488 of SEQ ID NO:14; or to residues 68-369 or 32-369 of SEQ ID NO:16; or to residues 1-305 of SEQ ID NO:18; or to residues 1-132 of SEQ ID NO:20; or to residues 29-320 of SEQ ID NO:22; or to residues 29-188 of SEQ ID NO:24; or to residues 301-625 or 30-625 of SEQ ID NO:26; or to residues 166-496 or 38-496 of SEQ ID NO:28; or to residues 26-361 of SEQ ID NO:30; or to residues 593-903 or 23-903 of SEQ ID NO:32 and retain the mannanase activity of the wild-type protein.

199

e

Please replace the paragraph on page 91, lines 22-25 with:

The two PCR primers used have the following sequences:

E9

LWN5494 5′-GTCGCCGGGGCGGCCGCTATCAATTGGTAACTGTATCTCAGC -3′ (SEQ ID NO: 35)

LWN5495 5′-GTCGCCCGGGAGCTCTGATCAGGTACCAAGCTTGTCGACCTGCAGAA TGAGGCAGCAAGAAGAT -3′ (SEQ ID NO: 36)

Please replace the paragraphs on page 92, lines 1-16 with:

This cloning replaces the first amyL promoter cloning with the same promoter but in the opposite direction. The two primers used for PCR amplification have the following sequences:

E10

#LWN5938 5`-GTCGGCGGCCGCTGATCACGTACCAAGCTTGTCGACCTGCAGAATG AGGCAGCAAGAAGAT -3′ (SEQ ID NO: 37)

#LWN5939 5`-GTCGGAGCTCTATCAATTGGTAACTGTATCTCAGC -3′ (SEQ ID NO: 38)

The plasmid pSJ2670 was digested with the restriction enzymes PstI and BclI and a PCR fragment amplified from a cloned DNA sequence encoding the alkaline amylase SP722 (Patent # WO 9526397-A1) was digested with PstI and BclI and inserted to give the plasmid pMOL944. The two primers used for PCR amplification have the following sequence:

#LWN7864 5` -AACAGCTGATCACGACTGATCTTTTAGCTTGGCAC-3′ (SEQ ID NO: 39)

#LWN7901 5` -AACTGCAGCCGCGGCACATCATAATGGGACAAATGGG -3′ (SEQ ID NO: 40)

Please replace the paragraph on page 97, lines 13-21 with:

The mannanase encoding DNA sequence of the invention was PCR amplified using the PCR primer set consisting of the following two oligo nucleotides:

E11

BXM2.upper.SacII

5'-GTT GAG AAA GCG GCC GCC TTT TTT CTA TTC TAC AAT CAC ATT ATC-3' (SEQ ID NO: 41)

200

e

E11

BXM2.core.lower.NotI

5'-GAC GAC GTA CAA GCG GCC GCT CAC TAC GGA GAA GTT CCT CCA TCA G-3' (SEQ ID NO: 42)

Please replace the paragraph on page 98, line 29 – page 99, line 9 with:

E12

One such positive clone was restreaked several times on agar plates as used above, this clone was called MB748. The clone MB748 was grown overnight in TY-10 µg/ml Kanamycin at 37°C, and next day 1 ml of cells were used to isolate plasmid from the cells using the Qiaprep Spin Plasmid Miniprep Kit #27106 according to the manufacturers recommendations for B. subtilis plasmid preparations. This DNA was DNA sequenced and revealed the DNA sequence corresponding to the mature part of the mannanase (corresponding to positions 94-990 of SEQ ID NO:1 and positions 32-330 of SEQ ID NO:2) with introduced stop codon replacing the amino acid residue no 331 corresponding to the base pair positions 1201-1203 in SEQ ID NO:1.

Please replace the paragraph on page 99, lines 13-21 with:

The mannanase encoding DNA sequence of the invention was PCR amplified using the PCR primer set consisting of these two oligo nucleotides:

BXM2.upper.SacII

E13

5'-CAT TCT GCA GCC GCG GCA AAT TCC GGA TTT TAT GTA AGC GG-3' (SEQ ID NO: 43)

BXM2.lower.NotI

5'-GTT GAG AAA GCG GCC GCC TTT TTT CTA TTC TAC AAT CAC ATT ATC -3' (SEQ ID NO: 44)

Please replace the paragraph on page 103, lines 8-9 with:

E14

The following N-terminal sequence of the purified protein was determined: ANSGFYVSGTTLYDANG (amino acids 32-48 of SEQ ID NO: 2).

201

e

Please replace the paragraphs on page 104, line 28 – page 105, line 8 with:

The pMB993 vector contains the CipB CBD with a peptide linker preceeding the CBD. The linker consists of the following peptide sequence ASPEPTPEPT (SEQ ID NO: 49) and is directly followed by the CipB CBD. The AS amino acids are derived from the DNA sequence that constitutes the Restriction Endonuclease site NheI, which in the following is used to clone the mannanse of the invention.

E15

Mannanase.Upper.SacII

5'-CAT TCT GCA GCC GCG GCA AAT TCC GGA TTT TAT GTA AGC GG -3' (SEQ ID NO: 45)

Mannanase.Lower.NheI

5'-CAT CAT GCT AGC TGT AAA AAC GGT GCT TAA TCT CG -3' (SEQ ID NO: 46)

Please replace the paragraphs on page 109, lines 1-6 with:

Mannanase.upper.SacII

5'-CAT TCT GCA GCC GCG GCA GCA AGT ACA GGC TTT TAT GTT GAT GG-3' (SEQ ID NO: 47)

E16

Mannanase.lower.NotI

5'-GAC GAC GTA CAA GCG GCC GCG CTA TTT CCC TAA CAT GAT GAT ATT TTC G -3' (SEQ ID NO: 48)

Please replace the paragraph on page 116, lines 21-24 with:

BXM1.upper.SacII

E17

5'- CAT TCT GCA GCC GCG GCA TTT TCT GGA AGC GTT TCA GC-3' (SEQ ID NO: 50)

BXM1.lower.NotI

5'-CAG CAG TAG CGG CCG CCA CTT CCT GCT GGT ACA TAT GC -3' (SEQ ID NO: 51)

202

e.

Please replace the paragraph on page 122, lines 23-28 with:

BXM5.upper.SacII

5'-CAT TCT GCA GCC GCG GCA CAT CAC AGT GGG TTC CAT G-3' (SEQ ID NO: 52)

BXM5.lower.NotI

5'-GCG TTG AGA CGC GCG GCC GCT TAT TGA AAC ACA CTG CTT CTT TTA G-3' (SEQ ID NO: 53)

Please replace the paragraph on page 126, lines 16-20 with:

BXM7.upper.SacII

5'-CAT TCT GCA GCC GCG GCA AGT GGA CAT GGG CAA ATG C-3' (SEQ ID NO: 54)

BXM7.lower.NotI

5'-GCG TTG AGA CGC GCG GCC GCT TAT TTT TTG TAT ACA CTA ACG ATT TC-3' (SEQ ID NO: 55)

Please delete the previously submitted Sequence Listing and insert the attached Sequence Listing (pages 1-56) at the end of the specification.

IN THE CLAIMS:

Please cancel claims 46-73 without prejudice or disclaimer. Please add new claims 74-106:

74. An isolated mannanase, which is

(a) a polypeptide encoded by the mannanase encoding part of the DNA sequence cloned into the plasmid present in *Escherichia coli* DSM 12197, or

(b) a polypeptide comprising a sequence of amino acids 32-330 or amino acids 32-490 of SEQ ID NO:2 or a fragment thereof that has mannanase activity, or

(c) a polypeptide encoded by a DNA sequence that hybridizes with nucleotides 94-990 or 94-1470 of SEQ ID NO:1 under high stringency conditions, or